

SEQUENCE LISTING

<110> Estell, David
Harding, Fiona

<120> Mutant Proteins Having Lower Allergenic Responses in
Humans and Methods for Constructing, Identifying and
Producing Such Proteins

<130> GC 527-D2

<140> 09/255,502
<141> 1993-02-23

<160> 7

<170> PatentIn Ver. 2.0

<210> 1
<211> 1494
<212> DNA
<213> *Bacillus amyloliquefaciens*

<220>
<221> CDS
<222> (96)..(1244)

<220>
<221> mat_peptide
<222> (417)..(1241)

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ttattctgca aatgaaaaaa aggagaggat aaaga gtg aga ggc aaa aaa gta 113
Val Arg Gly Lys Lys Val
-105

tgg atc agt ttg ctg ttt gct tta gcg tta atc ttt acg atg gcg ttc 161
Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu Ile Phe Thr Met Ala Phe
-100 -95 -90

ggc agc aca tcc tct gcc cag gcg gca ggg aaa tca aac ggg gaa aag 209
Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys
-85 -80 -75 -70

aaa tat att gtc ggg ttt aaa cag aca atg agc acg atg agc gcc gct 257
Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met Ser Ala Ala
-65 -60 -55

aag aag aaa gat gtc att tct gaa aaa ggc ggg aaa gtg caa aag caa 305
Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Gln
-50 -45 -40

ttc aaa tat gta gac gca gct tca gct aca tta aac gaa aaa gct gta 353
Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr Leu Asn Glu Lys Ala Val
-35 -30 -25

aaa gaa ttg aaa aaa gac ccg agc gtc gct tac gtt gaa gaa gat cac Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His -20	-15	-10	401
gta gca cat gcg tac gcg cag tcc gtg cct tac ggc gta tca caa att Val Ala His Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile -5	-1	1	449
aaa gcc cct gct ctg cac tct caa ggc tac act gga tca aat gtt aaa Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys 15	20	25	497
gta gcg gtt atc gac agc ggt atc gat tct tct cat cct gat tta aag Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys 30	35	40	545
gta gca ggc gga gcc agc atg gtt cct tct gaa aca aat cct ttc caa Val Ala Gly Gly Ala Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln 45	50	55	593
gac aac aac tct cac gga act cac gtt gcc ggc aca gtt gcg gct ctt Asp Asn Asn Ser His Gly Thr His Val Ala Gly Thr Val Ala Ala Leu 60	65	70	641
aat aac tca atc ggt gta tta ggc gtt gcg cca agc gca tca ctt tac Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr 80	85	90	689
gct gta aaa gtt ctc ggt gct gac ggt tcc ggc caa tac agc tgg atc Ala Val Lys Val Leu Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile 95	100	105	737
att aac gga atc gag tgg gcg atc gca aac aat atg gac gtt att aac Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn 110	115	120	785
atg agc ctc ggc gga cct tct ggt tct gct gct tta aaa gcg gca gtt Met Ser Leu Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val 125	130	135	833
gat aaa gcc gtt gca tcc ggc gtc gta gtc gtt gcg gca gcc ggt aac Asp Lys Ala Val Ala Ser Gly Val Val Val Ala Ala Ala Gly Asn 140	145	150	881
gaa ggc act tcc ggc agc tca agc aca gtc ggc tac cct ggt aaa tac Glu Gly Thr Ser Gly Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr 160	165	170	929
cct tct gtc att gca gta ggc gct gtt gac agc agc aac caa aga gca Pro Ser Val Ile Ala Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala 175	180	185	977
tct ttc tca agc gta gga cct gag ctt gat gtc atg gca cct ggc gta Ser Phe Ser Ser Val Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val 190	195	200	1025

tct atc caa agc acg ctt cct gga aac aaa tac ggg gcg tac aac ggt Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly 205 210 215	1073
acg tca atg gca tct ccg cac gtt gcc gga gcg gct gct ttg att ctt Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Leu Ile Leu 220 225 230 235	1121
tct aag cac ccg aac tgg aca aac actcaa gtc cgc agc agt tta gaa Ser Lys His Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu 240 245 250	1169
aac acc act aca aaa ctt ggt gat tct ttc tac tat gga aaa ggg ctg Asn Thr Thr Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu 255 260 265	1217
atc aac gta cag gcg gca gct cag taa aacataaaaa accggccttg Ile Asn Val Gln Ala Ala Ala Gln 270 275	1264
ccccggccgg ttttttattt ttcttcctcc gcatgttcaa tccgctccat aatcgacgga 1324 tggctccctc tggaaatttt aacgagaaac ggcgggttga cccggctcaag tcccgtaacg 1384 gccaagtccct gaaacgtctc aatcgccgct tcccggttgc cggcagctc aatgcccgtaa 1444 cggtcggcgg cggtttccctg ataccgggag acggcattcg taatcgatc 1494	

<210> 2
<211> 382
<212> PRT
<213> *Bacillus amyloliquefaciens*

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Ile Phe Thr Met Ala Phe Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly 20 25 30	
Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met 35 40 45	
Ser Thr Met Ser Ala Ala Lys Lys Asp Val Ile Ser Glu Lys Gly 50 55 60	
Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr 65 70 75 80	
Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala 85 90 95	
Tyr Val Glu Glu Asp His Val Ala His Ala Tyr Ala Gln Ser Val Pro 100 105 110	
Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr	

115	120	125
Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser		
130	135	140
Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala Ser	Met Val Pro Ser	
145	150	155
Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His Gly	Thr His Val Ala	
165	170	175
Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly Val	Leu Gly Val Ala	
180	185	190
Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu Gly	Ala Asp Gly Ser	
195	200	205
Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp	Ala Ile Ala Asn	
210	215	220
Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro	Ser Gly Ser Ala	
225	230	235
Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala Ser	Gly Val Val Val	
245	250	255
Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly Ser	Ser Ser Thr Val	
260	265	270
Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala Val	Gly Ala Val Asp	
275	280	285
Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val Gly	Pro Glu Leu Asp	
290	295	300
Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu	Pro Gly Asn Lys	
305	310	315
Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser Pro	His Val Ala Gly	
325	330	335
Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Trp	Thr Asn Thr Gln	
340	345	350
Val Arg Ser Ser Leu Glu Asn Thr Thr Lys Leu Gly	Asp Ser Phe	
355	360	365
Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala	Gln	
370	375	380

<210> 3
<211> 275
<212> PRT
<213> Bacillus subtilis

<400> 3

Ala Gln Ser Val Pro Tyr Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu
1 5 10 15

His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
20 25 30

Ser Gly Ile Asp Ser Ser His Pro Asp Leu Asn Val Arg Gly Gly Ala
35 40 45

Ser Phe Val Pro Ser Glu Thr Asn Pro Tyr Gln Asp Gly Ser Ser His
50 55 60

Gly Thr His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly
65 70 75 80

Val Leu Gly Val Ser Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
85 90 95

Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
100 105 110

Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
115 120 125

Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala Val Ser
130 135 140

Ser Gly Ile Val Val Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly
145 150 155 160

Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala
165 170 175

Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala
180 185 190

Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
195 200 205

Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr
210 215 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Thr
225 230 235 240

Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr
245 250 255

Leu Gly Asn Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
260 265 270

Ala Ala Gln
275

<210> 4
<211> 274

<212> PRT

<213> *Bacillus licheniformis*

<400> 4
Ala Gln Thr Val Pro Tyr Gly Ile Pro Leu Ile Lys Ala Asp Lys Val
1 5 10 15
Gln Ala Gln Gly Phe Lys Gly Ala Asn Val Lys Val Ala Val Leu Asp
20 25 30
Thr Gly Ile Gln Ala Ser His Pro Asp Leu Asn Val Val Gly Gly Ala
35 40 45
Ser Phe Val Ala Gly Glu Ala Tyr Asn Thr Asp Gly Asn Gly His Gly
50 55 60
Thr His Val Ala Gly Thr Val Ala Ala Leu Asp Asn Thr Thr Gly Val
65 70 75 80
Leu Gly Val Ala Pro Ser Val Ser Leu Tyr Ala Val Lys Val Leu Asn
85 90 95
Ser Ser Gly Ser Gly Ser Tyr Ser Gly Ile Val Ser Gly Ile Glu Trp
100 105 110
Ala Thr Thr Asn Gly Met Asp Val Ile Asn Met Ser Leu Gly Gly Ala
115 120 125
Ser Gly Ser Thr Ala Met Lys Gln Ala Val Asp Asn Ala Tyr Ala Arg
130 135 140
Gly Val Val Val Val Ala Ala Ala Gly Asn Ser Gly Asn Ser Gly Ser
145 150 155 160
Thr Asn Thr Ile Gly Tyr Pro Ala Lys Tyr Asp Ser Val Ile Ala Val
165 170 175
Gly Ala Val Asp Ser Asn Ser Asn Arg Ala Ser Phe Ser Ser Val Gly
180 185 190
Ala Glu Leu Glu Val Met Ala Pro Gly Ala Gly Val Tyr Ser Thr Tyr
195 200 205
Pro Thr Asn Thr Tyr Ala Thr Leu Asn Gly Thr Ser Met Ala Ser Pro
210 215 220
His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Leu
225 230 235 240
Ser Ala Ser Gln Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Tyr Leu
245 250 255
Gly Ser Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Glu Ala Ala
260 265 270
Ala Gln

<210> 5
<211> 269
<212> PRT
<213> *Bacillus lentinus*

<400> 5
Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
1 5 10 15
His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
20 25 30
Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
35 40 45
Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
50 55 60
His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
65 70 75 80
Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
85 90 95
Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
100 105 110
Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
115 120 125
Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
130 135 140
Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser
145 150 155 160
Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
165 170 175
Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
180 185 190
Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
195 200 205
Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
210 215 220
Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
225 230 235 240
Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
245 250 255
Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg

<210> 6
<211> 15
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Unknown Sequence

<400> 6
Ile Lys Asp Phe His Val Tyr Phe Arg Glu Ser Arg Asp Ala Gly
1 5 10 15

<210> 7
<211> 1052
<212> PRT
<213> Homo sapiens

<400> 7
Met Lys Leu Val Asn Ile Trp Leu Leu Leu Val Val Leu Leu Cys
1 5 10 15
Gly Lys Lys His Leu Gly Asp Arg Leu Glu Lys Lys Ser Phe Glu Lys
20 25 30
Ala Pro Cys Pro Gly Cys Ser His Leu Thr Leu Lys Val Glu Phe Ser
35 40 45
Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe
50 55 60
Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser
65 70 75 80
Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp
85 90 95
Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala
100 105 110
Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro
115 120 125
Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Pro Thr
130 135 140
Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg
145 150 155 160
Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala
165 170 175
Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln
180 185 190

Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln Met Gly Tyr Thr
195 200 205

Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys
210 215 220

His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu
225 230 235 240

Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val
245 250 255

Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu
260 265 270

His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp
275 280 285

Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Ile Asp Val Leu
290 295 300

Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp
305 310 315 320

Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile
325 330 335

Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln
340 345 350

Met Asp Val Ile Gly Val Gly Ile Asp Phe Glu Asp Asn Ile Ala
355 360 365

Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly Gly Tyr
370 375 380

Gly Arg Met Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly
385 390 395 400

Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala
405 410 415

Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln
420 425 430

Lys Arg Glu Leu Val Asn Pro Ala Ser Met Lys Gln Ala Leu Ile Ala
435 440 445

Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly
450 455 460

Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Asn Ser Tyr Lys Pro
465 470 475 480

Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys Pro Tyr
485 490 495

Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met Pro Thr
500 505 510

Val Val Asn Val Thr Ile Leu Asn Gly Met Gly Val Thr Gly Arg Ile
515 520 525

Val Asp Lys Pro Asp Trp Gln Pro Tyr Leu Pro Gln Asn Gly Asp Asn
530 535 540

Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp Pro Trp Ser Gly
545 550 555 560

Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu
565 570 575

Gly Ile Ala Gln Gly His Val Met Ile Thr Val Ala Ser Pro Ala Glu
580 585 590

Thr Glu Ser Lys Asn Gly Ala Glu Gln Thr Ser Thr Val Lys Leu Pro
595 600 605

Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg Val Leu
610 615 620

Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly Tyr Phe Pro Arg
625 630 635 640

Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp Asn Gly Asp His
645 650 655

Ile His Thr Asn Phe Arg Asp Met Tyr Gln His Leu Arg Ser Met Gly
660 665 670

Tyr Phe Val Glu Val Leu Gly Ala Pro Phe Thr Cys Phe Asp Ala Ser
675 680 685

Gln Tyr Gly Thr Leu Leu Met Val Asp Ser Glu Glu Tyr Phe Pro
690 695 700

Glu Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn Gly Leu Ser Leu
705 710 715 720

Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met Arg Lys Val Lys
725 730 735

Phe Tyr Asp Glu Asn Thr Arg Gln Trp Trp Met Pro Asp Thr Gly Gly
740 745 750

Ala Asn Ile Pro Ala Leu Asn Glu Leu Leu Ser Val Trp Asn Met Gly
755 760 765

Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Thr Leu Ala Asn His Asp
770 775 780

Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe Pro Glu Asp Gly
785 790 795 800

Val Val Ile Thr Gln Thr Phe Lys Asp Gln Gly Leu Glu Val Leu Lys
805 810 815

Gln Glu Thr Ala Val Val Glu Asn Val Pro Ile Leu Gly Leu Tyr Gln
820 825 830

Ile Pro Ala Glu Gly Gly Arg Ile Val Leu Tyr Gly Asp Ser Asn
835 840 845

Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp Leu Leu Asp
850 855 860

Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro Pro Ser Leu Ser
865 870 875 880

His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Ser Val Thr
885 890 895

Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu
900 905 910

Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro
915 920 925

Arg Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser
930 935 940

Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp Leu Asp Lys Val
945 950 955 960

Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser
965 970 975

Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met Pro Gly
980 985 990

Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val Phe Ala Phe Leu
995 1000 1005

Gly Ala Met Val Val Leu Ala Phe Phe Val Val Gln Ile Asn Lys Ala
1010 1015 1020

Lys Ser Arg Pro Lys Arg Arg Lys Pro Arg Val Lys Arg Pro Gln Leu
1025 1030 1035 1040

Met Gln Gln Val His Pro Pro Lys Thr Pro Ser Val
1045 1050